

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2002, 09:30:18 ; Search time 54 Seconds
(without alignments)
1896.853 Million cell updates/sec

Title: US-09-765-034-2
Perfect score: 1747
Sequence: 1 MGLMANNATCKNMLAAEA.....KSLTFSRMAHELLISPREK 334

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ .p2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US09765034/runat_05122002.132012.21343/app.query.fasta_1.519
-DB=Issued Patents NA -ORMT=faslap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCAIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09765034@cgn.1.1_17@runat.05122002.132012.21343 -NCPD=6 -ICPD=3
-NO.XIPYX -NO.MMAP -LARGQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1725	98.7	1996	2	US-08-559-524A-1
2	1725	98.7	1996	2	US-08-749-707-1
3	368.5	21.1	984	3	US-08-513-974B-41
4	368.5	21.1	1020	3	US-08-513-974B-370
5	358.5	20.5	984	3	US-08-513-974B-57
6	358.5	20.5	1023	3	US-08-513-974B-379
7	355	20.3	1842	1	US-08-442-134A-1
8	355	20.3	1842	1	US-08-444-581B-1
9	355	20.3	1842	1	US-08-446-088A-1
10	353.5	20.2	984	3	US-08-459-046-1
11	353.5	20.2	1578	4	US-09-044-404A-1
12	348	19.9	1643	1	US-08-383-750-3

13	348	19.9	1643	3	US-08-352-678-3	Sequence 3, Appli
14	348	19.9	1643	3	PCT-US93-09636-3	Sequence 3, Appli
15	345	19.7	1200	5	PCT-US92-02977-1	Sequence 1, Appli
16	342	19.6	2055	3	US-08-487-748A-3	Sequence 3, Appli
17	342	19.6	2055	3	US-08-480-070C-3	Sequence 3, Appli
18	342	19.6	2055	3	US-08-829-525-3	Sequence 3, Appli
19	342	19.6	2055	4	US-08-609-583A-3	Sequence 3, Appli
20	342	19.6	2055	4	US-08-937-399-3	Sequence 3, Appli
21	342	19.6	2055	4	US-09-310-367-3	Sequence 3, Appli
22	342	19.6	2055	4	US-09-032-337-3	Sequence 3, Appli
23	338	19.3	1106	5	PCT-US92-02977-5	Sequence 5, Appli
24	338	19.3	1106	5	PCT-US95-03032-4	Sequence 4, Appli
25	338	19.3	1200	5	PCT-US95-03032-1	Sequence 1, Appli
26	338	19.3	1510	1	US-07-759-568-8	Sequence 4, Appli
27	338	19.3	1748	1	US-08-202-056-8	Sequence 8, Appli
28	338	19.3	1901	1	US-08-153-848-43	Sequence 43, Appli
29	338	19.3	1901	3	US-09-299-843A-43	Sequence 43, Appli
30	338	19.3	1901	4	US-09-088-337B-43	Sequence 43, Appli
31	338	19.3	1901	5	PCT-US93-11153-43	Sequence 43, Appli
32	338	19.3	2453	5	PCT-US95-07180-1	Sequence 1, Appli
33	335.5	19.2	1224	2	US-08-742-440A-1	Sequence 1, Appli
34	334.5	19.1	1301	3	US-08-467-948A-7	Sequence 7, Appli
35	334.5	19.1	1301	3	US-08-467-947A-7	Sequence 7, Appli
36	333.5	19.1	1255	1	US-08-097-938-3	Sequence 3, Appli
37	333.5	19.1	1255	1	US-08-476-000-3	Sequence 3, Appli
38	333.5	19.1	1255	1	US-08-472-840-3	Sequence 3, Appli
39	333.5	19.1	1255	2	US-08-476-976-3	Sequence 3, Appli
40	333.5	19.1	1255	3	US-08-474-410-3	Sequence 3, Appli
41	333.5	19.1	1255	4	US-08-486-673B-3	Sequence 3, Appli
42	331	18.9	1176	5	PCT-US95-03032-2	Sequence 2, Appli
43	331	18.9	1883	1	US-08-202-036-2	Sequence 2, Appli
44	331	18.9	1933	1	US-08-076-093A-1	Sequence 1, Appli
45	331	18.9	1933	1	US-08-410-451-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-559-524A-1
; Sequence 1, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7176
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1996 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 625..1626
US-08-559-524A-1

Alignment Scores:
Pred. No.: 5.62e-176 Length: 1996
Score: 1725.00 Matches: 331
Percent Similarity: 99.10% Conservative: 0
Best Local Similarity: 99.10% Mismatches: 3
Query Match: 98.74% Indels: 0
DB: Gaps: 0

US-09-765-034-2 (1-334) x US-08-559-524A-1 (1-1996)

QY 1 MetleuglylIleMetAlaTPAsnAlaThrcyslysaSntPleuAlaIaIaAla 20
DB 625 ATGCTGGGATCATGCGATGGAATGCAACTTGCAAAAAGTGGCGAGAGGCTGCC 684

QY 21 LeuglulysTYTYrleuSerllePheTYrGlylleGluPheValIaGlyValleugly 40
DB 685 CTGGAAGAAGTACTACCTTTCATTTTATGAGATTGAGTTCGTTGGGAGCTCTTGA 744

QY 41 AsnThrIleValIaTYrGlyTYrIlePheSerleuIysAsnTPAsnSerSera 60
DB 745 AATACCATTTGTTTACGGCTACATCTTCTCTGAGAACTGGAAACAGCATATAT 804

QY 61 TyrlleuPheAsnleuSerValSerAsnleuAlaPheleuCYSThrleuProMetleu 80
DB 805 TATCTCTTAACCTCTGCTCTGACTTACCTTTCTGTCACCTCCCTCCATGCTGATA 864

QY 81 ArgSerTYrAlaAsnGlyAsnTPrlleTYrGlyAspValleuCYsIleSerAsnArgTYr 100
DB 865 AGGAGTTATGCGCATGGAATGATATGAGAGCGCTGCTGATAGACAGCATAT 924

QY 101 ValIeuhIsAlaAsnleuTYrThSerlleuPheleuThrPheIleSerIleAspArg 120
DB 925 GTGCTTCATGCGCAACCTTATACAGCATCTTCTTCTCATTTTATACGATATGATGA 984

QY 121 TyrlleuIleIleIysTYrProPheArgGluHisleuGlnIysValGluPheAlaIle 140
DB 985 TACTTGATATTAAGTATCCTTTCGAGAACACCTTTCGCAAAAGAAAGATTTGCTATT 1044

QY 141 LeuIleSerleuAlaIleTPrValleuValIleThrleuGluIleuProIleleuProleu 160
DB 1045 TTATTCCTCTGGCCATTTGGGTTTAGTATACCTTAGAGTTACTACCATCTCCCTT 1104

QY 161 IleAsnProValIleIleThraspAsnGlyThrThrcysAsnAspPheAlaSerSerGlyAsp 180
DB 1105 ATAATATCCTGTTATATACGACAAATGCGCACCTGTAATGATTTTGCAAATTCGAGAAC 1164

QY 181 ProAsnTYrAsnleuIleTYrSerMetCysleuThrleuGlnIysPheleuIleProleu 200
DB 1165 CCCAATCAACCTCATTTACAGCATGCTTAACTGTTGGGGTCTTATTCCTCTT 1224

QY 201 PheValMetCysPhePheTYrTYrIysIleAlaIleuPheleuIysGlnIysArgAsnArgGln 220
DB 1225 TTGTGATGTTCTTTCTTTATACAGATGCTCTCTCCATAAGAGAGAGATAGAGAG 1284

QY 221 ValAlaThrAlaIleuProleuGluIysProleuAsnleuValIleMetAlaValIle 240
DB 1285 GTTGTCTACTGCTGCGCCCTTGAAAGCCTCTCAACTGGTCATCATGCGAGTGAATC 1344

QY 241 PheSerValProPheThrProTYrHisValMetArgAsnValArgIleAlaSerArgIleu 260
DB 1345 TTCTCTGTGCTTTTACACCTATACAGCTATGCGGAATGAGAGATGCTTCACGCTG 1404

QY 261 GlySerTPrllysGlnIysCYSThrGlnValIleIleAsnSerPheTYrIleValIleThr 280
DB 1405 GGGAGTTGGAAGAGTATGACTGACATGAGTCTCATCAACTCTTTTACATTGTGACA 1464

QY 281 ArgProleuAlaPheleuAsnSerValIleAsnProValIlePheTYrPheleuGlyAsp 300
DB 1465 CGGGCTTTGGCTTCTTCAACAGTCTCATCAACCTGCTCTTATTTCTTTGGAGAT 1524

QY 301 HisPheArgAspMetleuMetleuAsnGlnleuArgHisAsnPheIysSerleuThrSerPhe 320
DB 1525 CACTTCAGGAGCATGCTATGATGAACTGAGACCAACTTCATAATCCCTTACATCTCTT 1584

QY 321 SerArgTPrAlaHisGluIleuIleuSerPheArgGlyIys 344
DB 1585 AGCAGATGGCTCATGAACTCTCTTCTTCAATTCAGAGAAAG 1626

RESULT 2
US-08-749-707-1
Sequence 1, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Janlzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,707
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 625..1626
US-08-749-707-1

Alignment Scores:
Pred. No.: 5.62e-176 Length: 1996
Score: 1725.00 Matches: 331
Percent Similarity: 99.10% Conservative: 0
Best Local Similarity: 99.10% Mismatches: 3
Query Match: 98.74% Indels: 0
DB: Gaps: 0

US-09-765-034-2 (1-334) x US-08-749-707-1 (1-1996)

QY 1 MetleuglylIleMetAlaTPAsnAlaThrcyslysaSntPleuAlaIaIaAla 20
DB 625 ATGCTGGGATCATGCGATGGAATGCAACTTGCAAAAAGTGGCGAGAGGCTGCC 684

QY 21 LeuglulysTYTYrleuSerllePheTYrGlylleGluPheValIaGlyValleugly 40
DB 685 CTGGAAGAAGTACTACCTTTCATTTTATGAGATTGAGTTCGTTGGGAGCTCTTGA 744

```

Db      685 CTGGAAGACTACCTTCATTTTATNGGATGAGTTCGTGGGAGCTTGA 744
Qy      41 AsnThrIleValIleValIleValIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
Db      745 AATACCATGTTGTTTACGGCTACATCTCTCTGTAAGAACAAGCAACACTAATAT 804
Qy      61 TyrLeuPheAsnLeuSerValIleSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
Db      805 TATCTCTTAACCTCTCTCTGCTGACTTACCTTTCTGTCACCCCTCCCACTGCTGATA 864
Qy      81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
Db      865 AGGAGTATGACCAATGAAACTGATATATGAGAGCTGCTGCATAGCAACCCATAT 924
Qy      101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
Db      925 GTGCTTCATGCCAACCTCTATACAGCAATCTCTTCTCTCACTTTATCAGCATATGATGCA 984
Qy      121 TyrLeuIleIleIleTyrTrpProPheArgGlnHisLeuLeuGlnLysLysGluPheAlaIle 140
Db      985 TACTTGATTAATTAAGTATGCTTTCCAGAACACCTTCTGCAAAAGAAAGATTGCTAAT 1044
Qy      141 LeuIleSerLeuAlaIleTrpValLeuValIleLeuGluLeuLeuProIleLeuProLeu 160
Db      1045 TTATATCTCTGCGCATTTGGGTTTAGTACCTTAGTACCTTACCCATCTCCCTT 1104
Qy      161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
Db      1105 ATAAATCGTGTATTAACCTGACATGACACACCTCTGTAATGATTTTCCAACTTCTGAGAC 1164
Qy      181 ProAsnTyrAsnLeuLeuTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
Db      1165 CCCAACTACAACTCATTAACACCATGCTGTACACTGTGGGGTCTTATTCCTCT 1224
Qy      201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
Db      1225 TTGTGATGTTGTTCTTTATTTACAAAGATGCTCTCTCTTAAAGCAGAGGAATAGCGAG 1284
Qy      221 ValAlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValIle 240
Db      1285 GTTGCTACTGCTGCTGCCCTTGAAGCCCTGCAACTGTGTATTCATGCGAGTGTATG 1344
Qy      241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
Db      1345 TTCTCTGCTGTTTACACCCCTATCAGCTATCGGAAATGTGAGATCGCTTACCGCTG 1404
Qy      261 GlySerTyrLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
Db      1405 GGGAGTGGGAAGCATATCATGCTCAGTCACTGAGTGTCTCATCACTCTTTTACATTGAGACA 1464
Qy      281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
Db      1465 CGGGCTTTGGGCTTTCGAGACAGTGCATCAACCCCTCTTATTTCTTTTGGGAGAT 1524
Qy      301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPhelysSerLeuThrSerPhe 320
Db      1525 CACTTACGAGCACTGCTGATGAAATCAACGAGACAACTCAAACTCCCTTACATCTCTT 1584
Qy      321 SerArgTrpAlaHisGlnLeuLeuLeuSerPheArgGlnLys 334
Db      1585 AGCAGATGGGCTCATGAACTCCTACTTCTCATTCAGAGAAAG 1626

```

```

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-41
Alignment Scores:
Pred. No.: 1,42e-30
Score: 368.50
Percent Similarity: 48.58%
Best Local Similarity: 30.28%
Length: 984
Matches: 96
Conservative: 58
Mismatch: 128

```



```

QY 38 ValLeuGlyAsnThrIleValIleValIleValIlePheSerIleuysAsnTrpAsnSer 57
   ::: ||| ::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 CTGTGCTGTAACCGCGTGGCGCTTACATCTCTGTGGCGCTCAAGACCTGGAATGCG 257
QY 58 SerAsnIleTyrlleupheAsnleuSerValSerAspLeuAlaPheLeuGlyThrIlePro 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 TCCACCAACATATATGTTACACCGCTGGCTGTGTGATGCACATGATGCGGCTCCGTGCGG 317
QY 78 MetLeuIleArgSerTyrlleuAlaAsnGly---AsnTrpIleTyrlleuGlyAspValleuGly 96
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 318 CTGCTGTGCTATATACACCGCGCGGACACCTGACCTGACGACGAGGCTCTGCTGCAAG 377
QY 97 SerAsnArgTyrlleuAlaAsnleuTyrlleuSerIleuPheLeuThrPheIle 116
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 378 CTGGTGGCTTCTCTTACACCAACCTTACTGACGATCTCTCTCTCCACCTGACATC 437
QY 117 SerIleAspArgTyrlleuIleIleTyrlleuProPheArgIleuIleuIleuGly 136
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 438 AGCGTGCACCGGTGTGTGGCGCTTACGACCTGTGCGCTCCCTGCGCGTGGCGCGGCGC 497
QY 137 GluPheAlaIleLeuIleSerIleuAlaIleTrpValleuValThrIleuGluLeuPro 156
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 498 CGCTACGCTGCGCGCGGTGGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 557
QY 157 IleLeuProLeuIleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAla 176
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 558 GTGCTCTACTTGTCTACCC--ACCAGCGCGCGCGCGCGCTGACCTGCCACGACCTGCG 614
QY 177 SerSerGlyAspProAsnTyrlleuIleTyrlleuSerMetCysLeuThrIleuGlyPhe 196
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 615 GACCCGACGCTCTACGCGCGCTGTGCGCTACGCTACGCTACGCTGCGCGCTGTCTCTTC 674
QY 197 LeuIleProLeuPheValMetCysPhePheTyrlleuIleAlaLeuPheLeuGlyGln 216
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 675 GCGGTGCGCGCTTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 734
QY 217 ArgAsnArgGlnValAlaThrAlaLeuProLeuGluIleuGlyProLeuAsnleuValIleMet 236
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 735 CCAGCTACGCGGACCTCGCGCGCGCTGCTGACGCGGACGCGGACGCGGCGCGCGCACCATC 794
QY 237 AlaValValIle---IlePheSerValProPheThrProThrIleGluPheValMetArgAsnVal 254
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 795 GCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 854
QY 255 ArgIleAlaSerArgLeuGlySerTrpIleGlyGlnCys---ThrGlnValValIle 273
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 855 TACTACTCTCTGCGCTGCG---CTGAGACTCAGCTGCGGCGCACACCTCCACAGCGCATC 905
QY 274 AsnSerPheTyrlleuValIleThrArgProLeuAlaPheLeuAsnSerValIleAsnProVal 293
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 906 AACATGCGCTCAACAGGTACCCCG---CTGGCCAGTGTACAGTGTGCTGACCCCGTGG 962
QY 294 PheTyrlleuLeuGly 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 963 CTCTACTCTCTGCGTGG 980

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691156th Carolina
COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,088A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D. Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 57..1181
US-08-446-088A-1

Alignment Scores:
Pred. No.: 9,92e-29 Length: 1842
Score: 355.00 Matches: 102
Percent Similarity: 50.33% Conservative: 52
Best Local Similarity: 33.33% Mismatches: 134
Query Match: 20.32% Indels: 18
DB: 1 Gaps: 9

US-09-765-034-2 (1-334) x US-08-446-088A-1 (1-1842)
QY 7 TrpAsnAlaThrCysLys---AsnTrpLeuAlaIleGluAlaIleuGlu----- 22
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 TGGATGACACCATATGACGACCTGGAGGCGATGAGCTGCGCTACAGTCCGCTTC 137
QY 23 -----LysTyrlleuSerIlePheTyrlleuGluPheValIleGly 37
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 AACGAGGACTTCAAGTACGCTGCTGCTGTCTCTACAGGCGTGTGCTGCTGGG 197
QY 38 ValLeuGlyAsnThrIleValIleValIleValIlePheSerIleuysAsnTrpAsnSer 57
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 198 CTGTGCTGTAACCGCGTGGCGCTTACATCTCTGTGGCGCTCAAGACCTGGAATGCG 257
QY 58 SerAsnIleTyrlleupheAsnleuSerValSerAspLeuAlaPheLeuGlyThrIlePro 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 TCCACCAACATATATGTTACACCGCTGGCTGTGTGATGCACATGATGCGGCTCCGTGCGG 317
QY 78 MetLeuIleArgSerTyrlleuAlaAsnGly---AsnTrpIleTyrlleuGlyAspValleuGly 96
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 318 CTGCTGTGCTATATACACCGCGCGGACACCTGACCTGACGACGAGGCTCTGCTGCAAG 377
QY 97 SerAsnArgTyrlleuAlaAsnleuTyrlleuSerIleuPheLeuThrPheIle 116
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 378 CTGGTGGCTTCTCTTACACCAACCTTACTGACGATCTCTCTCTCCACCTGACATC 437
QY 117 SerIleAspArgTyrlleuIleIleTyrlleuProPheArgIleuIleuIleuGly 136
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 438 AGCGTGCACCGGTGTGTGGCGCTTACGACCTGTGCGCTCCCTGCGCGTGGCGCGGCGC 497

```


QY 311 ArgHisAsnPhenylSerLeuThrSerPheSerArgTrpAlaHisGluLeuLeuSer 330
DB 928 -----CGGCGAGCACATGAGTCTCTACAGAAA 954
QY 331 PheArgGluLys 334
DB 955 CTCACAGACAAA 966

RESULT 11
US-09-044-404A-1
; Sequence 1, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMB1 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH-70001-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1578 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-044-404A-1

Alignment Scores:
Pred. No.: 1.15e-28 Length: 1578
Score: 353.50 Matches: 91
Percent Similarity: 47.52% Conservative: 62
Best Local Similarity: 28.26% Mismatches: 152
Query Match: 20.23% Indels: 17
DB: 4 Gaps: 8

US-09-765-034-2 (1-334) x US-09-044-404A-1 (1-1578)
QY 8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaLeuGluLysTrpLeuSer 27
DB 497 TCTGCCACATGCGCATGACTATT-----GATGACTTCGCGCAATCAAGTGTATTCC 547

QY 28 IlePheTyGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyGly 47
DB 548 ACCTGTACTCATGATCTCTGTGTAGGCTTCTGGCAATGGCTTGTCTGTGC 607
QY 48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
DB 608 CTCATATAAAACCTATCAAGAAAGTCAAGCTTCCAAAGTATACATGATTATTAAGCAGTA 667
QY 68 SerAspLeuAlaPheLeuGlyThrLeuPheLeuIleArgSerTyrAlaAsn---Gly 86
DB 668 GCAGATCTACTTGTGTGTGACACATGCGCTCTCGTGTGTGTATATGTCACAAAGG 727
QY 87 AsnTrpIleTyrGlyAspValLeuGlyIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
DB 728 ATTTGGCTCTTGTGTGATCTTGTGTGCGCTGACACCATCTTGTGTATGCAATCC 787
QY 107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
DB 788 TATTGTAGCATCTTCTTATGACAGCCATGAGCTTTTCCGGTGCATTGCAATTTCTTTT 847
QY 127 ProPheArgGluHisLeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIle 146
DB 848 CCAGTCCAGAAACATTAATTGTTACACAGAAAGCCAGTTTGTGTGTAGGTATT 907
QY 147 TrpValLeuValThrLeuGluLeuProIleLeuProLeuIleAsnProValIleThr 166
DB 908 TGGATTTTGTGATTTGTGACCATGCTCTCTATGCGCAACCAACAAAGATGG 967
QY 167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp-----ProAsnTyr 183
DB 968 AAAAATAATACCAAGTGC-----TTTGAGCCCCCAACAGACATCAAACTAAATATCAT 1021
QY 184 AsnLeuIleTyrSerMetCysLeuThrLeuGlyPheLeuIlePro-----LeuPhe 201
DB 1022 GTTTGGTGTGATATGATGATGATGTTGTGTGTATATCAATCCCTTTTGTATTATA 1081
QY 202 ValMetCysPhePheTyrTyrIleAlaLeuPheLeuLysGlnArgAsnArgGlnVal 221
DB 1082 ATGTCTGTACCAATGATCATCTTGTACCTTCTAAATAAATCAATGAAAAAATCTG 1141
QY 222 AlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleLeuAlaValIlePhe 241
DB 1142 TCAGTGCAT-----AAAAAGGCTATAGATGATGATGATGATGATGATGATGATGAT 1192
QY 242 SerValProPheThrProTyrHisValMetArgValValArgIleAlaSerArgLeuGly 261
DB 1193 TTAGTCAAGTTTCAATGATATCATATTCACAGTACATTCACCTTATTTTACACAT 1252
QY 262 SerTrpLysGlnTyrGlnCysThrGlnValVal---IleAsnSerPheTyrIleValThr 280
DB 1253 GAACCTAAA-----CCCTGTGATCTGCTTGAATGAGAGATCCGGTGCATTAAC 1306
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
DB 1307 TTGTCTGTGGCTGATCCATTCATTTGCTTGTGACCCCTGCTATATTTCTTCTGTGGGG 1366
QY 301 HisPheArgAspMetLeuLeuGlnLeuArgHisAsnPhenylSerLeuThrSerPhe 320
DB 1367 AACTTTAGGAAGAGCTGTGTACATTTAGAAAGCATTTCTTGTCCAGCGTACTTATGTA 1426
QY 321 SerArg 322
DB 1427 CCCAGA 1432

RESULT 12
US-08-383-750-3
; Sequence 3, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8


```

Db 160 ATCATTTGGGCTGGGAACTTACTAGCCTTGTCGTCATTTCTTCAAAACAGAAAAA 219
Oy 55 TrpAsnSerSerAsnIleTyrIleuPheAsnLeuSerValSerAspLeuAlaPheLeuCys 74
Db 220 ATCAACTCTACCACTTATTCACAAATTTGGTATTCGATATATCTTTATTCACAG 279
Oy 75 ThrLeuPrometLeuIleArgSerTyrAlaAsnGly---AsnTyrIleTyrIleAspVal 93
Db 280 GCTTTGGCTACAGAAATACCTACTAGTGCATGCAATGGCGCTTTGAGGAAATCGAGATGCC 339
Oy 94 LeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleuPheLeu 113
Db 340 TTGCTAGAGATTAATCGCGTAGTGTATTACATCAACACATATGACGAGGTGAACTTTAG 399
Oy 114 ThrPheIleSerIleAspArgTyrIleuIleIleTyrTyrProPheArgIleHisLeu 133
Db 400 ACCCTCCCTGAGATTTGACCGCTTTCATGTGTGGTGCCACCTCTACGCTACCAAGATA 459
Oy 134 GlnLysLysGluPheAlaIleLeuIleSerLeuAlaIleTyrValLeuValThrLeuGlu 153
Db 460 AAAAGGATTTGAACATGCAAAAGGCGTGTGCATATTTGTGTGATTCATGATTTGCTCAG 519
Oy 154 LeuLeuProIleLeuProLeuIleAsnProValIleThrAspAsnGly-----ThrThr 171
Db 520 ACACCTCCACCTC-----CTCATCAACCTATGTCAAAGCAGAGGCTGAAGATTTACA 573
Oy 172 CysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeu 191
Db 574 TGCATGGAGTAT-----CCAAACTTGAAGAACTAAATCTCTCCCTCG 618
Oy 192 ThrLeuLeu-----GlyPheLeuIleProLeuPheValMetCysPhePhe 206
Db 619 ATTCGCTTTGGGGCATGTTTCTATAGGATATGACTTCCACTATATATCTTCTCATCTGC 678
Oy 207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db 679 TATTCCTGAGATCTGTCGCAACTCTTCAGAACTGCCAAACAA-----AACCCA 726
Oy 227 Leu-----GlnLysProLeuAsnLeuValIleMetAlaValVal 239
Db 727 CTCACCTGAGAAATCTGCTGTAAACAAAGGCTCTCAACACAAATATCTTATTTGTT 786
Oy 240 IlePheSerValProPheThrProTyrHisValMetArgAsnValArgIleLeuSerArg 259
Db 787 GTGTTTGTCTCTGTTTACACCTTACCAATGTTGCAATTAATCAACATATGTTAAGAG 846
Oy 260 LeuGlySerTyrLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIle--- 278
Db 847 CTTCGTTTCTGTAATTTCTCGAATGAGCCAA-----AGACATTCGTTCCAGATTTCT 900
Oy 279 -----ValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPhe 296
Db 901 CTGCATTTAGATGATGCTGATGAATCTCAATTCCTGATGAGCCCTTTTATCTACTTC 960
Oy 297 LeuLeuGlyAspHisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLys--- 315
Db 961 TTTGCATGTAAGGCTATTAAGAAAGGTTATGAGAGATGCTGAAGCGCAAGTCAAGTGT 1020
Oy 316 SerLeuThrSerPheSerArgTyrPalaHisGlu 326
Db 1021 TCGATTTCTAGTGTGCTGAGTACGCCCTGAA 1053

```

```

STREET: 225 Franklin Street
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02977
FILING DATE: 19920410
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/685,101
FILING DATE: April 10, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00231/051002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1200
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-02977-1

Alignment Scores:
Pred. No.: 6,36e-28 Length: 1200
Score: 345.00 Matches: 99
Percent Similarity: 44.02% Conservative: 63
Best Local Similarity: 26.90% Mismatches: 140
Query Match: 19.75% Indels: 66
DB: Gaps: 12

US-09-765-034-2 (1-334) x PCT-US92-02977-1 (1-1200)
Oy 1 MetLeuGlyIleMetAlaTrpAsnAlaThr---CysLysAsnTrpLeuAlaAlaGluAla 19
Db 105 GTAATGGAAGTAAACGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 164
Oy 20 Ala----- 20
Db 165 GCAAAATGCTACTGCTATGCTCTCTGTAGAAAAAGATTATAGCCCTGTGCTAGTCAACC 224
Oy 21 -----LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValAlaGlyVal 38
Db 225 CAGACACTTAACAAATATGTTGTGTGTCGTCATCATATGCCCTGTGCTCTGCTGAGCTG 284
Oy 39 LeuGlyAsnThrIleValAlaValTyrIleTyrIlePheSerLeuLysAsnTrpAsnSer 58
Db 285 CTGGGCAACTCCCTGCTGATGCTGCTCATCTGATGATGATGATGATGATGATGATGATGATG 344
Oy 59 AsnIleTyrIleuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuPromet 78
Db 345 GACGCTACCTGCTGAACCTGCGCCATGCGCAGCTGCTTTTGGCTTACCATGCGCTATTC 404
Oy 79 LeuIleArgSerTyrAlaAsnGlyAsnTyrIleTyrGlyIleAspValLeuCysIleSerAsn 98
Db 405 TGGCGCGCTCTCAAGCAAGAAAGCG---TGCATTTTGGCAGCAGCCCTGTGCAAGTGGGG 461
Oy 99 ArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIle 118
Db 462 TCGCTGTGAAGGAAGTCACTTCTACGATGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 521
Oy 119 AspArgTyrLeuIleIleIleTyrProPheArgGlnHisLeuGlnLysLysGluPhe 138

```

```

RESULT 15
PCT-US92-02977-1
Sequence 1, Application PC/TUS9202977
GENERAL INFORMATION:
APPLICANT: Navarro, Javier et al.
TITLE OF INVENTION: INTERLEUKIN-8 RECEPTORS AND
RELATED MOLECULES AND
METHODS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson

```


THIS PAGE BLANK (USPTO)